

# FIGURE 1

TABLE 1

Exon-Intron Boundary Sequences of the Human alpha-7 nAChR Subunit Gene

Exon Number	Exon length(bp)	cDNA position	splice acceptor	flanking exon sequence	splice donor	Intron number	Intron Size approximate (Kb)
1	55	1-55		...CTG CAC G	GTAAAGCCAC	1	0.3
2	140	56-195	TCTCCTTAAG	TG TCC.....GAC GTG L H V S D V	GTGAGTCCCG	2	Unknown
3	45	196-240	TTTTTTGAAG	GAT GAG.....CAA ATG D E Q M	GTAAGTTAAG	3	9.0
4	110	241-350	TGTGTGTCAG	TCT TGG.....AAC AG S W N S	GTAAGCATAT	4	Unknown
5	80	351-430	CTGTTTCTAG	T GCT GAT.....CCT CCA G A D P P	GTAAGCTGCA	5	4.0
6	168	431-598	ACCCACACAG	GC ATA.....CTA GTG G G I L V	GTAAGCCATG	6	1.0
7	195	599-793	CCCTATGGAG	GA ATC.....TCC CTG G G I S L	GTAAGCGCCC	7	1.0
8	87	794-880	TATGTTTTAG	GG ATA.....TTG ATA G G I L I	GTAAGGCAAG	8	3.5
9	110	881-990	CTCTCCACAG	CC CAG.....AAG TGG A Q K W	GTACGTTCTT	9	5.0
10	519	991-1509	GTCTCCCCAG	ACC AGA... T R			

FIGURE 2

TABLE 2  
Sequence Variants Identified in Full-Length and Duplicated Genomic Clones

DNA	EXONS CONT.	EXON 6 +/- 497-498	EXON 7 654	EXON 7 690	EXON 10 1269	EXON 10 1335	L76630
CHR15 HYBRID	5-10 1-10	+TG -TG			C/C		6GT 8GT
YAC							
D-948a10	5-10	-TG	T				6GT
D-853b12	6-10	-TG	T	A	C		6GT
D/F	5-10						
969b11	1-10	+TG -TG	C/T	G/A	C/T	C/C	6GT 8GT
F-134h10	1-10	+TG	C				8GT
F-776a12	1-10	+TG	C				8GT
F-791e6	1-10	+TG	C				8GT
F-811b6	1-10	+TG	C				8GT
F-953g6	1-10	+TG	C				8GT
F-859c11	1-10	+TG	C				8GT
F-810f11	1-10	+TG	C				8GT
F-801e1	1-10	+TG	C				8GT
BAC							
F-467o18	1-10	+TG	C				8GT

DNA	Control #	EXON 6 +/- 497-498	EXON 7 654	EXON 7 690	EXON 10 1269	EXON 10 1335
Control Genomic DNA	43	+/+ 10 +/- 33 -/- 0	C/C 5 C/T 38 T/T 0	G/G 0 G/A 43 A/A 0	C/C 6 C/T 36 T/T 1	C/C 24 C/T 19 T/T 0

# FIGURE 3

TABLE 3  
Expression Analysis of Sequence Variants

Subj	Bases 497-498			Base 654			Base 690			Base 933			Base 1296			Base 1335		
	DNA	1-10 cDNA	5-10 cDNA	DNA	1-10 cDNA	5-10 cDNA	DNA	1-10 cDNA	5-10 cDNA	DNA	1-10 cDNA	5-10 cDNA	DNA	1-10 cDNA	5-10 cDNA	DNA	1-10 cDNA	5-10 cDNA
SL061	+/-	+	+/-	CT	C	CT	GA	G	GA	G	G	G	CT	CT	CT	C	C	C
SL084	+	+	+	C	C	C	GA	G	GA	G	G	G	CT	C	CT	C	C	C
SL111	+/-	+	+/-	CT	C	CT	GA	G	GA	G	G	G	CT	CT	CT	CT	CT	CT
SL097	+	+	+	CT	C	CT	GA	G	GA	G	G	G	CT	C	CT	C	C	C
SL089	+	+	+	C	C	C	GA	GA	GA	GA	GA	GA	CT	CT	CT	C	C	C
SHSY	+/-	+	+/-	CT	C	CT	GA	GA	GA	GA	GA	GA	C	C	C	C	C	C

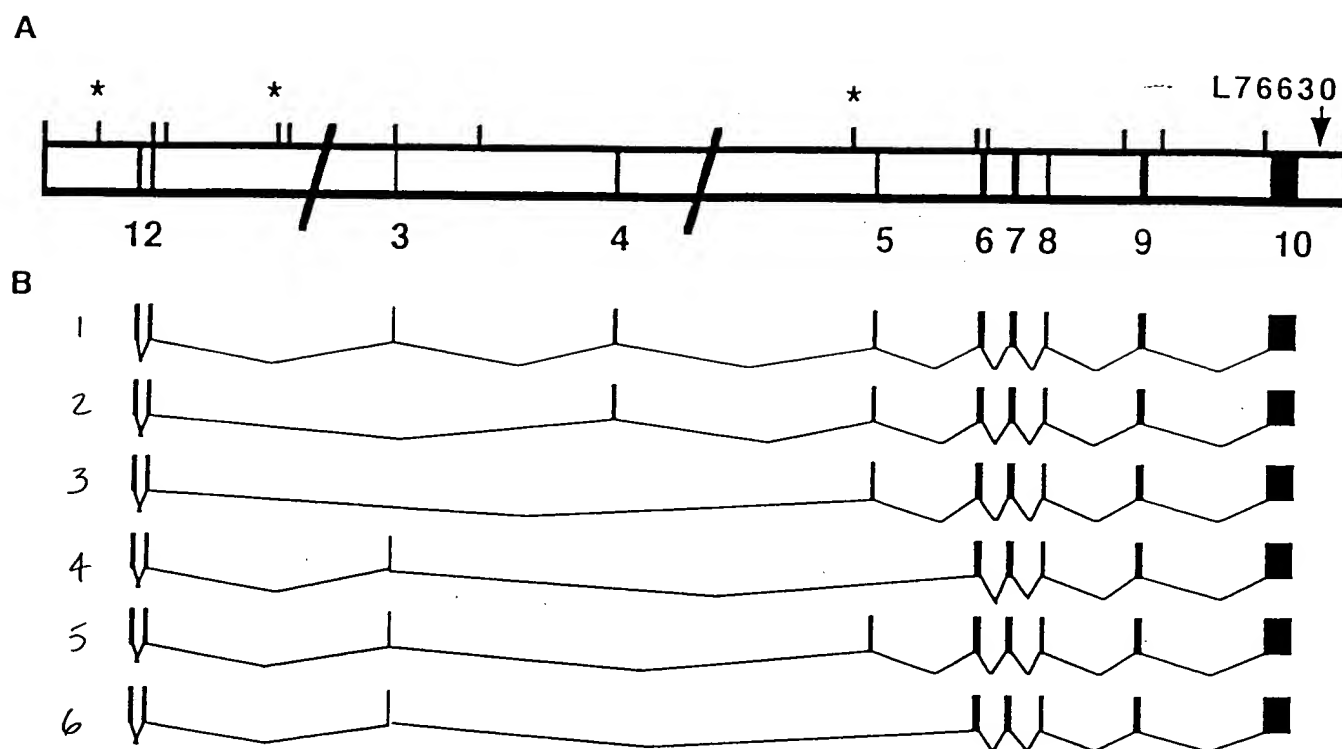


[illegible]

FIGURE 6

	1						
<b>EXON D</b>	CAGGCCGCCA	CATAGCTCCC	GCCAAGTCCT	CGGTGCCCCCT	TGCCATTTTC	CAGCCGCGTC	CCACGAGGGT
297bp	CACGGCGGCG	GGGAGAGGTG	GAGCCGCGAG	AGCTCGGCCG	GGGGCCCCGC	CTGGTGCCCG	CGGCCATGAC
	AGCGGCTCGG	GACTGGCTCC	TTTTCCGCGC	CCCTCCCCGC	GGAGGTGAGG	GGAAGATGTC	CATGTCAGGG
	TTCAAGGCCA	AACCGAAGTT	ACTGGCCTCT	ATCTTCCAGG	AGAACCAGGA	GCCACAGCCG	CGGCTCACGC
	CCCACCGCAA	CATTAAGgtg	agtcgcc.....				
		297					
		298					
<b>EXON C</b>	....ctc	atttcagATT	ACAAGTGGAC	ACCTGAGTCA	GCAGGACCTG	GAATCCCAGA	TGAGAGAGCT
125bp	TATCTACACG	ACTCAGATCT	TGTGTGCACC	CCCATTATTG	ACAATCCAAA	GGTGCAGAAA	GCACTCTGAC
	AAgtgagttg	ta.....					
	422						
		423					
<b>EXON B</b>	..ttaaccac	agATAATGAA	ACAACCACCA	TCGGTTAAAT	TTGATGCAAA	AATATTGCAT	CTACCAGCAT
64bp	TTTCAGgtag	gatcat.....					
	486						
		487					
<b>EXON A</b>	.....ttta	ttctagTTCC	AATTGCTAAT	CCAGCATTTG	TGGATAGCTG	CAAACCTGCGA	TATgtaagta
47bp	aca.....						533
		534					
<b>EXON 5</b>	...ctgtttc	tagTGCTGAT	GAGCGCTTTG	ACGCCACATT	CCACACTAAC	GTGTTGGTGA	ATTCTTCTGG
80bp		GCATTGCCAG	TACCTGCCTC	CAGgtaagctgca.....			
				613			
		614					
<b>EXON 6</b>	....accaca	cagGCATATT	CAAGAGTTCC	TGCTACATCG			
27bp				640			

FIGURE 7



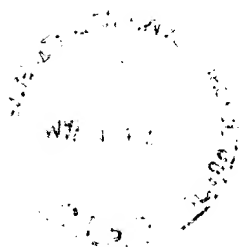
## FIGURE 8

1 agaacgcaag ggagaggtag agcctggcct tgggcagccc ctggcctggc cagaggcgcg  
61 aggccgagag cccgctcggt ggagactggg ggtggaggtg cccggagcgt acccagcgcc  
121 gggagtacct cccgctcaca ctcggggctg cagttccctg ggtggccgcc gagacgctgg  
181 cccgggctgg agggatggcg gggcggggac gggggcgggg gcggggctcg tcacgtggag  
241 aggcgcgcgg gggcggggcg ggcgggggcg cgcgcccggc tccttaaagg cgcgcgagcc  
301 gagcggcgag gtcctctgt ggccgcaggc gcaggcccgg gcgacagccg agacgtggag  
361 cgcgccggct cgctgcagct ccgggactca ac



## FIGURE 9

1 agccctttcc caggcggtag cggggggcagt ggtgctgtg cccttttaa ctgcggcttg  
61 acgggagccg cgcctcctgt cgggtggagtc ggttataaag ggagcagccc cgcaggccgc  
121 cacatagctc cgcceaagtc ctcggtgccc ctgccattt tccagccgcg ctcccacgag  
181 ggtcacggcg gcggggagag gtggagccgc gagagctcgg ccggggggccc cgcctggtgg  
241 ccgcgggccat gacagcggct cgggactggc tccttttcg cggccctccc gccggaggtg  
301 aggggaagat gtccatgtca ggggtcaagg ccaaaccgaa gttactggcc tctatcttc  
361 aggagaacca ggagccacag ccgcggctca cggccaccg caacattaag attacaagt  
421 gacacctgag tcagcaggac ctggaatccc agatgagaga gcttatctac acgactcaga  
481 tcttgtgtc accccatta ttgacaatcc aaaggtgcag aaagcactct gacaattcca  
541 attgctaate cagcatttgt ggatagctgc aaactgcgat attgctgatg agcgtttga  
601 cgccacattc cacactaacg tgttggtgaa ttctctggg cattgccagt acctgcctcc  
661 aggcatatc aagagttcct gctacatcg



## FIGURE 10

1 caggccgcca catagctccc gccaaagtcct cgggtgcccct tgccatttc cagccgcgct  
61 cccacgaggg tcacggcggc ggggagaggt ggagccgcga gagtcggcc gggggccccg  
121 cctggtggcc gcggccatga cagcggtcgc ggactggctc ctttccgcg cccctcccgc  
181 cggaggtgag ggggaagatgt ccatgtcagg gttaaggcc aaaccgaagt tactggcctc  
241 tatcttcag gagaaccagg agccacagcc gcggctcacg cccaccgca acattaagat  
301 tacaagtga cacctgagtc agcaggacct ggaatcccag atgagagagc ttatctacac  
361 gactcagatc ttgtgtcac cccattatt gacaatcaa aggtgcagaa agcactctga  
421 caaataatga aacaaccacc atcgggttaa tttgatgaa aaatattgca tctaccagca  
481 tttcagttc caattgctaa tccagcattt gtggatagct gcaaactgcg atattgctga  
541 tgagcgctti gacgccacat tccacactaa cgtgttggtg aattctctg ggcattgcca  
601 gtacctgcct ccaggcata tcaagagttc ctgctacac g